

57. (Amended) A method of enriching for and identifying nucleic acid sequence differences with respect to a reference sequence comprising:

- Sub D1*
- a) fragmenting a nucleic acid sample from one or more individuals;
 - b) physically separating a subset of said nucleic acid fragments based on the size of the fragments;

f2

- c) operatively linking said subset of step (b) with an oligonucleotide or a vector;

- d) replicating said operatively linked subset to form an enriched collection of replicated molecules; and

- e) detecting one or more nucleotide sequence differences in the members of said collection of step (d) with a method that detects one or more nucleotide differences with respect to a reference sequence,

wherein steps (a)-(e) enrich for and identify a nucleic acid sequence difference with respect to a reference sequence.

Sub D2

69. (Amended) A method of enriching for and identifying nucleic acid sequence differences with respect to a reference sequence comprising:

- a) fragmenting a nucleic acid sample from one or more individuals;

f3

- b) physically separating a subset of said nucleic acid fragments based on the size of the fragments;

- c) detecting one or more nucleic acid sequence differences with respect to a reference sequence in the members of said separated molecules of step (b), wherein steps (a)-(c) enrich for and identify a nucleic acid sequence difference with respect to a reference sequence.

Kindly enter new claims 157 and 158 as follows:

Sub D3

f4

157. (New) A method of enriching for and identifying a nucleic acid sequence difference with respect to a reference sequence comprising: